

**Supplemental Table 4:
Peptides of viral proteins co-purified by the Strep-NP (vRNP components)**

Protein	Peptides*	Probability**	
Polymerase basic protein 1 (PB1)	R.NQPAATALANTIEVFR.S	0.9983	
	R.ALTLNTMTKDAER.G	0.9775	
	R.SIC[160]EKLEQSGLPVGGNEK.K	0.9920	
	K.AGLLVSDGGPNLYNIR.N	0.9933	
	R.GFVYFVETLAR.S	0.9162	
	R.AIATPGM[147]QIRGFVYFVETLAR.S	0.9517	
	R.GILEDEQM[147]YQK.C	0.9073	
	R.TQIPAEM[147]LASIDLK.Y	0.9529	
	R.M[147]FLAM[147]ITYITR.N	0.9937	
	K.NM[147]EYDAVATTHSWIPKR.N	0.9913	
	K.NMEYDAVATTHSWIPKR.N	0.9988	
	R.GILEDQQMYQK.C	0.9318	
	R.TQIPAEM[147]LASIDLKYFNDSTR.K	0.9257	
	R.TQIPAEMLASIDLKYFNDSTR.K	0.9321	
	Polymerase acidic protein (PA)	R.NYFTAEVSHC[160]R.A	0.9172
		R.LFTIRQEMASR.G	0.9737
		R.AYVDGFEPNGYIEGK.L	0.9742
K.QVLAELQDIENEKIPR.T		0.9778	
R.LADQSLPPNFSSLENFR.A		0.9721	
R.AYVDGFKPNGYIEGK.L		0.9083	
K.YC[160]VLEVGDMD[147]LLR.S		0.9771	
Polymerase basic protein 2 (PB2)	R.VM[147]VSPLAVTWWNR.N	0.9417	
	R.LNPMHQLLR.H	0.9697	
	K.ANVLIGQGDVVLVM[147]KR.K	0.9999	
	R.NDDVDQSLIIAAR.N	0.9821	
	R.YGPALSINELSNLAK.G	0.9606	
	K.M[147]EFEPFQSLVPK.A	0.9695	
	R.LKHGTFGPVHFR.N	0.9257	
	K.LLPFAAAPPK.Q	0.9606	
	K.IRVHEGYEFTM[147]VGR.R	0.9931	
	K.QSGM[147]QFSSLTINVR.G	0.9946	
	R.ILTSESQLTSTTK.E	0.9635	
	R.ILTSESQLTSTTKEK.K	0.9985	
	R.LTVLGKDAGPLTEDPDEGTAGVESAVLR.G	0.9957	
	Nucleoprotein	R.MC[160]SLMQGSTLPR.R	0.9172
K.GKFQTAAQR.A		0.9331	
R.M[147]VLSAFDER.R		0.9963	

R.GVFELSDEK.A	0.9546
K.GVGTM[147]VM[147]ELIR.M	0.9642
R.SGAAGAAVKGVGTM[147]VM[147]ELIR.M	0.9573
K.SQLVWM[147]AC[160]HSAAFEDLR.V	0.9968
R.LIQNSITIER.M	0.9726
R.EGYSLVGIDPFR.L	0.9876
K.LLQNSQVYSLIRPNENPAHK.S	0.9981
R.LIQNSLTIER.M	0.9853
R.SYEQM[147]ETDGERQNATEIR.A	0.9934
R.ASSGQISIQPTFSVQR.N	0.9999
R.ESRNPNGNAEFEDLIFLAR.S	0.9999
R.NLPFDRPTIMAAFTGNTEGR.T	0.9989
R.NPGNAEFEDLIFLAR.S	0.9989
R.SGGNTNQQRASSGQISIQPTFSVQR.N	0.9956
R.LMESARPEDVSFQGR.G	0.9666
K.ATSPIVPSFDM[147]SNEGSYFFGDNAEEYDN.	0.9979
R.IMESARPEDVSFQGR.G	0.9551

* dots after the first and before the last amino acid indicate the site of tryptic digestion, numbers between rectangular brackets show modified molecular weights.

** Peptide probabilities were calculated with Peptide Prophet with a cut off value of 0.9 (Keller et al. 2002, Ref. 22).